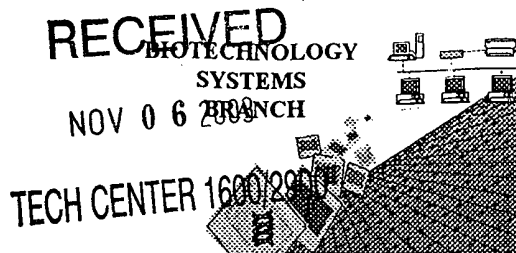


## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/595,947D

Source: 1/600

Date Processed by STIC: 10/27/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003



1600

## RAW SEQUENCE LISTING

DATE: 10/27/2003

PATENT APPLICATION: US/09/595,947D

TIME: 09:29:14

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

5 <110> APPLICANT: ICARD-LIEPKALNS, Christine  
 6 MALLET, Jacques  
 7 RAVASSARD, Philippe  
 9 <120> TITLE OF INVENTION: POLYPEPTIDES OF THE "BASIC-HELIX-LOOP-HELIX" bHLH  
 10 FAMILY, CORRESPONDING NUCLEIC ACID SEQUENCES  
 12 <130> FILE REFERENCE: P26,952 USA  
 14 <140> CURRENT APPLICATION NUMBER: US 09/595,947D  
 15 <141> CURRENT FILING DATE: 2000-06-16  
 17 <150> PRIOR APPLICATION NUMBER: FR96/15651  
 18 <151> PRIOR FILING DATE: 1996-12-19  
 20 <150> PRIOR APPLICATION NUMBER: PCT/FR97/02368  
 21 <151> PRIOR FILING DATE: 1997-12-19  
 23 <150> PRIOR APPLICATION NUMBER: US 09/331,356  
 24 <151> PRIOR FILING DATE: 1999-07-12  
 26 <160> NUMBER OF SEQ ID NOS: 40  
 28 <170> SOFTWARE: PatentIn Ver. 3.1

*pp 1-2, 4-9*  
**Does Not Comply**  
**Corrected Diskette Needed**

## ERRORED SEQUENCES

129 <210> SEQ ID NO: 5  
 130 <211> LENGTH: 18  
 131 <212> TYPE: DNA  
 132 <213> ORGANISM: Artificial Sequence  
 134 <220> FEATURE:  
 135 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR Primers  
 137 <400> SEQUENCE: 5 cgcggtgtcc tgcccacc 18  
 E--> 137 5 cgcggtgtcc tgcccacc 18 *← move this under <400> 5 line*  
 164 <210> SEQ ID NO: 8  
 165 <211> LENGTH: 214  
 166 <212> TYPE: PRT  
 167 <213> ORGANISM: Rattus norvegicus *p.2*  
 169 <400> SEQUENCE: 8  
 170 Met Ala Pro His Pro Leu Asp Ala Pro Thr Ile Gln Val Ser Gln Glu  
 171 1 5 10 15  
 173 Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser  
 174 20 25 30  
 176 Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu  
 177 35 40 45  
 179 Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg  
 180 50 55 60  
 182 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln  
 183 65 70 75 80

## RAW SEQUENCE LISTING

DATE: 10/27/2003

PATENT APPLICATION: US/09/595,947D

TIME: 09:29:14

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

```

185 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
186      85      90      95
E--> 188 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
E--> 189      100      105      110
191 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
E--> 192      115      120      125
194 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
E--> 195      130      135      140
197 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
E--> 198 145      150      155      160
200 Pro Gly Gly Gly Ser Ser Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
E--> 201      165      170      175
203 Ser Gln Ala Gly Ser Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
E--> 204      180      185      190
206 Gly Leu Gln Val Pro Ser Ser Pro Ser Cys Leu Leu Pro Gly Thr Leu
E--> 207      195      200      205
209 Val Phe Ser Asp Phe Leu
E--> 210      210
266 <210> SEQ ID NO: 10
267 <211> LENGTH: 214
268 <212> TYPE: PRT
269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 10
272 Met Thr Pro Gln Pro Ser Gly Ala Pro Thr Val Gln Val Thr Arg Glu
273 1      5      10      15
275 Thr Glu Arg Ser Phe Pro Arg Ala Ser Glu Asp Glu Val Thr Cys Pro
276      20      25      30
278 Thr Ser Ala Pro Pro Ser Pro Thr Arg Thr Pro Gly Asn Cys Ala Glu
279      35      40      45
281 Ala Glu Glu Gly Gly Cys Arg Gly Ala Pro Arg Lys Leu Arg Ala Arg
282      50      55      60
284 Arg Gly Gly Arg Ser Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
285 65      70      75      80
287 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
288      85      90      95
290 His Asp Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
291      100      105      110
293 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
294      115      120      125
296 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
297      130      135      140
E--> 299 Ser Leu Tyr Ala Leu Glu Pro Pro Ala Pro His Cys Gly Glu Leu Gly
300 145      150      155      160
302 Ser Pro Gly Gly Pro Pro Gly Asp Trp Gly Ser Leu Tyr Ser Pro Val
303      165      170      175
304 Ser Gln Ala Gly Ser Leu Ser Pro Ala Ala Ser Leu Glu Glu Arg Pro
305      180      185      190
307 Gly Leu Leu Gly Ala Thr Ser Ser Ala Cys Leu Ser Pro Gly Ser Leu
308      195      200      205

```

see p. 4

for explanation

OK - These  
numbers are  
in bold print  
due to above  
error

use "L" not "I"  
several "I"

Glu  
==

## RAW SEQUENCE LISTING

DATE: 10/27/2003

PATENT APPLICATION: US/09/595,947D

TIME: 09:29:14

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

310 Ala Phe Ser Asp Phe Leu  
311 210

09/595,947D 4

<210> 8  
 <211> 214  
 <212> PRT  
 <213> Rattus norvegicus

<400> 8

Met	Ala	Pro	His	Pro	Leu	Asp	Ala	Pro	Thr	Ile	Gln	Val	Ser	Gln	Glu
1				5					10					15	
Thr	Gln	Gln	Pro	Phe	Pro	Gly	Ala	Ser	Asp	His	Glu	Val	Leu	Ser	Ser
			20					25					30		
Asn	Ser	Thr	Pro	Pro	Ser	Pro	Thr	Leu	Val	Pro	Arg	Asp	Cys	Ser	Glu
		35					40					45			
Ala	Glu	Ala	Gly	Asp	Cys	Arg	Gly	Thr	Ser	Arg	Lys	Leu	Arg	Ala	Arg
	50					55					60				
Arg	Gly	Gly	Arg	Asn	Arg	Pro	Lys	Ser	Glu	Leu	Ala	Leu	Ser	Lys	Gln
65				70					75					80	
Arg	Arg	Ser	Arg	Arg	Lys	Lys	Ala	Asn	Asp	Arg	Glu	Arg	Asn	Arg	Met
				85					90				95		
His	Asn	Leu	Asn	Ser	Ala	Leu	Asp	Ala	Leu	Arg	Gly	Val	Leu	Pro	Thr
		100						105					110		

What does this mean? Is it a  
 typographical error? If it represents  
 a gap, then the amino acids following  
 it must be in a new sequence ID No.,  
 and the <160> response must be  
 changed.

09/595,947D 5

<210> 13  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 13  
atcggttgaga ctggtaccag cagagtcacg agagagacta cacggtactg nnnnnnnnnn 60

see p. 6 for env  
explanation

6

VARIABLE LOCATION SUMMARY

DATE: 10/27/2003

PATENT APPLICATION: US/09/595,947D

TIME: 09:29:15

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

*error explanation*

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:2; N Pos. 9,16

Seq#:13; N Pos. 52,53,54,55,56,57,58,59,60

*See p. 7 for more errors*

09/595,9420 ?

<210> 26

<211> 15

<212> DNA

<213> Artificial Sequence

<220> ~~<223>~~ *insert a hard return* Description of Artificial Sequence: Probe

<400> 26

aggaagctcc gggca 15

<210> 27

<211> 1381

*<2127>* <212> RNA

<213> Artificial Sequence

*hard return*  
<220> <223> Description of Artificial Sequence: Probe

<400> 27

*no  
spaces  
within  
bracket*



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/595,947D

DATE: 10/27/2003

TIME: 09:29:15

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10272003\I595947D.raw

L:100 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:2  
 L:100 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:2  
 L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
 L:137 M:301 E: (44) No Sequence Data was Shown, SEQ ID:5  
 L:137 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:0 SEQ:5  
 L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
 M:332 Repeated in SeqNo=8  
 L:210 M:252 E: No. of Seq. differs, <211> LENGTH:Input:214 Found:213 SEQ:8  
 L:299 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:347 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:13  
 L:347 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:13  
 L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
 L:499 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
 L:501 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>  
 ORGANISM:Artificial Sequence  
 L:501 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:501  
 L:510 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
 L:512 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>  
 ORGANISM:Artificial Sequence  
 L:512 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:512